

Fig 1

SEQ ID NO.1

7th amino acid sequence of ATCC 71529 ank

SEQ ID NO.2

```

1  GTGGCCCTGGTCGTACAGAAATATGGCGGTTCTCGCTTGACAGTGCGGAACGATTAGA
-----+-----+-----+-----+-----+-----+-----+-----+-----+ 60
    P A L V V O N Y G G S S L E S P L P L R
61  AACGTGCGCTGAACGGATCGTTGCCACCAAGAGGCTCGAAAAGATGTCGTGGTGTCTGC
-----+-----+-----+-----+-----+-----+-----+-----+-----+ 120
    N V A E R I V A T K K A G N D V V V V C
121 TCCGCARTGGGAGACACCACGGATGAACCTTCTAGAACTTGCAGCGGCAGTGAATCCCGTT
-----+-----+-----+-----+-----+-----+-----+-----+-----+ 180
    S A M G D T T D E L L E L A A A V N P V
CCGCCAGCTCGTGAAATGGATATGCTCCTGACTGCTGGTGAGCGTATTTCTAACGCTCTC
181 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 240
    P P A R E M D M L L T A G E R I S N A L
GTCGCCATGGCTATTGAGTCCCTTGGCGCAGAAGCTCAATCTTTCAGTGGCTCTCAGGCT
241 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 300
    V A M A I E S L G A E A Q S F T G S Q A
GGTGTGCTCACCACCGAGCGCCACGGAACGCACGCATTGTTGACGTCACACCGGGTCGT
301 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 360
    G V L T T E R H G N A R I V D V T P G R
GTGCGTGAAGCACTCGATGAGGGCAAGATCTGCATTGTTGCTGGTTTTTCAGGGTGTTAAT
361 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 420
    V R E A L D E G K I C I V A G F Q G V N
AAAGAAACCCGCGATGTCACCACGTTGGGTGCTGGTGGTCTGACACCACTGCAGTTGCG
421 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 480
    K E T R D V T T L G R G G S D T T A V A
TTGGCAGCTGCTTTGAACGCTGATGTGTGTGAGATTTACTCGGACGTTGACGGTGTGTAT
481 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 540
    L A A A L N A D V C E I Y S D V D G V Y
ACCGCTGACCCGCGCATCGTTCTAATGCACAGAAGCTGGAAAAGCTCAGCTTCGAAGAA
541 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 600
    T A D F R I V P N A Q K L E K L S F E E
ATGCTGGAACCTTGCTGCTGTTGGCTCCAAGATTTTGGTGCTGCGCAGTGTGAATACGCT
601 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 660
    M L E L A A V G S K I I V L R S V E Y A
CGTGCATTCAATGTGCCACTTCGCGTACGCTCGTCTTATAGTAATGATCCCGGCACTTTG
661 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 720
    R A F N V P L R V R S S Y S N D P G T L
ATTGCCGGCTCTATGGAGGATATTCCTGTGGAAGAAGCAGTCCTTACGGGTGTGCAACC
721 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 780
    I A G S M E D I P V E E A V L T G V A T
GACAAGTCCGAAGCCAAAGTAACCGTTCTGGGTATTTCCGATAAGCCAGGCGAGGCTGCC
781 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 840
    D K S E A K V T V L G I S D K P G E A A

```

Fig 2A

30x
114

SEQ ID No:1
(cont)

1841 AAGGTTTTCCGTGCGTTGGCTGATGCAAAATCAACATTGACATGGTTCTCAGAACGTC 900

SEQ ID No:2
(cont)

901 K V F R A L A D A E I N I D M V L D N V

TCCTCTGTGGAAGACGGCACCACCGACATCAGGTTACCTGCCCTCGGGGTGACGGACGGC 960

S S V E D G T T D E T F T C P R A D G R

CGTGCGATGGAGATCTTGAAGAAGCTTCAGGTTCAAGGCAACTGGACCAATGTGCTTTAC 1020

R A M E I L K K L Q V Q G N W T N V L Y

GACGACCAGGTCGGCAAAGTCTCCCTCGTGGGTGCTGGCATGAAGTCTCACCAGGTGTT 1080

D D Q V G K V S L V G A G M K S H P G V

ACCGCAGAGTTCATGGAAGCTCTGCGCCATGTCAACSTGAACATCGAATTGATTTCCATC 1140

T A E F M E A L R E V N V K I E L I S I

TCTGAGATCCGCATTTCCGTGCTGATCCSTGAAGATGATCTGGATGCTGCTGCACGTGCA 1200

S E I R I S V L I R E D D L D A A A K A

TTGCATGAGCAGTTCCAGCTGGCGCGGCGLAGACGAAGCCGTCGTTTATGCAGGCACCGGA 1260

L H E Q F Q L G G E D E A V V Y A T T C

CGCTAA
1261 ----- 1266

R *

Fig 2B

amino acid sequence of PTC 21529 asd

SEQ ID NO: 3

SEQ ID NO: 4

```
ATGAGCACCATCGCAGTTGTTGGTGCACCCGGCCAGGTCCGGCCAGGTTATGCCACAGTTT 60
-----
N T T I A V V G A T G Q V G Q V H R T F
TTGGAAGAGCGCAATTTCCGAGCTGACAGTGTTCGTTTCTTTGCTTCCCGCGTTCCGCA 120
61 -----
L E E R N F P A D T V R F F A S P R S A
GGCCGTAGATTGAATTCGGTCCGACCGGAATCGAGGTAGAAGACATTACTCAGGCAACC 180
121 -----
G R K I E F R G T E I E V E D I T O A T
GAGGACTCCCTCAAGGGCATCGACGTTGCGTTGTTCTCTGCTGGAGGCACCGCTTCCAAG 240
181 -----
E E S L K G I D V A L F S A G G T A S K
CAGTACGCTCCACTGTTTGTCTGCTGACGGCTGACTGTTGTGCATAACTCTCTGCTTGG 300
241 -----
Q Y A F L F A A A G A T V V D N S S A W
CGCAAGGACGACAGGTTCCACTAATCGTCTGTGAGGTGAACCGTTCCGACAAGGATTCC 360
301 -----
R K D D E V P L I V S E V N P S D K D S
CTGGTCAAGGCAATTATTCCGAATCTTAATGACACCATGGCTGCAATGCCAGTGGTG 420
361 -----
L V K G I I A N P R C T T H A A M P V L
AAGCCACTGACAGATGCCGCTGGTCTTGTAAAGCTTACGTTTCTCTTACCAGCGTGT 480
421 -----
K P L R Q A A G L V K L H V S S Y Q A V
TCCCGTTCTGGTCTTGCAGGTGTGCAAACTTGGCAAAGCAGGTTGCTGCAGTTGGCGAC 540
481 -----
S G S G L A C V E T L A K Q V A A V G D
CACACCGTTGAGTTGCTCCATGATGGACGCTGCTGACGACGCGATGTGGACCTTAC 600
541 -----
H N V E F V H D C Q A A D A G D V G P Y
GTTTCCCAATCGCTTACAACGTCCTGCCATTCCCGGGAACCTCTGATGACGGCACC 660
601 -----
V S P I A Y R V L P F A G N L V D U G T
TTCGAAACCGACGAAGAGCAGAAGCTGCCCAACGAATCCCGGAAGATTCTCGGCTCCCA 720
661 -----
F E T D E E Q K L R N E S R K I L G L P
GACCTCAAGGTCTCAGGCACCTCGCTCCGCTGCCGGTTTTCACCGGCCACACGCTGACC 780
721 -----
D L K V S G T C V R V P V F T G H T L T
ATTACGCGCAATTCGACAAAGCAATCAGCTGACGACGCGCAGGAGATCTTGGGTGCC 840
781 -----
I H A E F D K A I T V E Q A Q E I L G A
GCTTCAGGCGTCGAGCTTGTGACGTCGCAACCCCACTTCCAGCTCCCGGCATTGACGAA 900
841 -----
A S G V E L V D V P T P L A A A G I D E
```

Fig 3A

SEQ ID NO:3
(cont)

901 TCCCTCGTTGGACGCATCCGTCAGGACTCCACTGTCGACGACAACCGCGGTCTGGTTCTC 960

Seq ID NO:4
(cont)

S L V G R I R Q D S T V D D N K G L V L
961 GTCGTATCTGGCGATAACCTTCGCAAGGGCGCAGCACTGAACACCATTTCAGATTGCTGAG 1020

V V S G D N L R K G A A L N T I Q I A E

CTGCTGGTTAAGTAA
1021 -----+----- 1035

L L V K *

Fig 3B

Amino acid sequence of dapB

SEQ ID NO: 5 ATGGGAATCAAGGTTGGCGTTCTCGGAGCCAAAGGCCGTGTTGGTCAAACCTATTGTGGCA
1 -----+-----+-----+-----+-----+-----+ 60

SEQ ID NO: 6 M G I K V G V L G A K G R V G Q T I V A
GCAGTCAATGAGTCCGACGATCTGGAGCTTGTTCAGAGATCGGCGTCCGACGATGATTTC
61 -----+-----+-----+-----+-----+-----+ 120
A V N E S D D L E L V A E I G V D D D L
AGCCTTCTGGTAGACAACGGCGCTGAAGTTGTCTGTTGACTTCACCACTCCTAACGCTGTG
121 -----+-----+-----+-----+-----+-----+ 180
S L L V D N G A E V V V D F T T P N A V
ATGGGCAACCTGGAGTTCTGCATCAACAACGGCATTCTGCGGTTGTTGGAACCACGGGC
181 -----+-----+-----+-----+-----+-----+ 240
M G N L E F C I N N G I S A V V G T T G
TTCGATaATGCTCGTTTGGAGCAGGTTGCGGcCTGGCTTGAAGGAAAAGACAATGTCTGGT
241 -----+-----+-----+-----+-----+-----+ 300
F D N A R L E Q V R A W L E G K D N V G
GTTCTGATCGCACCTAACTTTGCTATCTCTGCGGTGTTGACCATGGTCTTTTCCAAGCAG
301 -----+-----+-----+-----+-----+-----+ 360
V L I A P N F A I S A V L T M V F S K Q
GCTGCCCGCTTCTTCGAATCAGCTGAAGTTATTGAGCTGCACCACCCCAACAAGCTGGAT
361 -----+-----+-----+-----+-----+-----+ 420
A A R F F E S A E V I E L H H P N K L D
GCACCTTCAGGCACCGCGATCCACACTGCTCAGGGCATTGCTGCGGCACGCAAAGAAGCA
421 -----+-----+-----+-----+-----+-----+ 480
A P S G T A I H T A Q G I A A A R K E A
GGCATGGACGCACAGCCAGATGCGACCGAGCAGGCACTTGAGGGTTCCCGTGGCGCAAGC
481 -----+-----+-----+-----+-----+-----+ 540
G M D A Q P D A T E Q A L E G S R G A S
GTAGATGGAATCCCgGTTCAcGCAGTCCGCATGTCCGGCATGGTTGCTCACGAGCAAGTT
541 -----+-----+-----+-----+-----+-----+ 600
V D G I P V H A V R M S G M V A H E Q V
ATCTTTGGCACCCAGGGTCAGACCTTGACCATCAAGCAGGACTCCTATGATCGCAACTCA
601 -----+-----+-----+-----+-----+-----+ 660
I F G T Q G Q T L T I K Q D S Y D R N S
TTTGCACCAGGTGTCTTGGTGGGTGTGCGCAACATTGCACAGCACCCAGGCCTAGTCGTA
661 -----+-----+-----+-----+-----+-----+ 720
F A P G V L V G V R N I A Q H P G L V V
GGACTTGAGCAATTACCTAGGCCTGTAA
721 -----+-----+-----+-----+-----+ 747
G L E H Y L G L *

Fig 4

SEQ ID NO: 8

ATTTATTTGGTGTATCTCGACCGGAAAGTGGCCACGCTATTTTGGAGCTTACAAAGAAC
 60
 H F F G F L D Q U S A T T I L E D Y K N
 ATTAACCAACATCTGGGTAGCTATCTTGGCTACCGAAAGCTGGGACCCAGCTCTCGMAAAG
 120
 H T N I F V A I V G Y C H L G R S V E K
 CTTATTGCCAAGCAGCGCCGACATCGACCTTGTAGGAATCTTCTCGCGCCGGCCCAACCGTC
 180
 L I A K Q P D H O L V G I F S R R A T L
 GACCAAAAGACGCCAGTCTTTGATGTCCCGGACCTGGACAAGCACCGCCGACGCTGGAG
 240
 D T K T P V E D V A D V D K H A O D V D
 GTGCTGTCTCTGTGCATGGGCTCGCCACCGACATCCCTGAGCAGGACCCAAAGTTCGGG
 300
 V L F L C H G S A T D I P E Q A P K F A
 CAGTTCGCCTGCACCGTAGACACCTACGACAACCAACCGGACATCCCAAGCCACCGCCAG
 360
 Q F A C T V O T Y D N H R D I P R T R Q
 GTCATGAAGCAAGCGCCACCGCAGCGCGCAACGTTGCACTGGTCTCTACCTGGCTGGGAT
 420
 V M N E A A T A A C N V A L V S T S W D
 CCAGGAATGTCTCCATCAACCGCGTGTACGCAGCGGCACTCTTAGCCGAACACCAAGCAG
 480
 P G H F S I N R V Y A A A V L A E H O Q
 CACACCTTCTGGGGCCGAGCTTTGTACAGGGCCACTCCGATCTTTGCCAAGCATCCCT
 540
 H T F H G P G L S Q G H S D A L R E I P
 GGCCTTCAAAAGGCGCTCCAGTACACCCCTCCCATCCGAAGAAGCCCTGGCAAGAGGCCCGG
 600
 G T Q K A V Q Y T L P S E E A L E H A R
 CGTCCGAAGCGCGGACCTACCGGAAGCAACCCACAAGCCCAATCTTTCGTGGTT
 660
 R G E A G D L T G K Q T H K R Q C F V V
 CCGGAAGCGCGGAGCAGGAGCGCATCGAAACGACATCCGACCATCCCTGATTACTTC
 720
 A D A A D H E R I E N D I R T H F D Y F
 GTTGGGTACGAAGTCGAAGTCAACTTCATCGACGAAGCAACCTTGGAGCTTACGACACAC
 780
 V G Y E V E V N F I D E A T L D A E H T
 GGCATGCCACACGGGGAACAGTGATCACCACCGGGGACACCGGTGGCTTACACGACAC
 840
 G M P H G G H V I T T C D T G C F N H T
 GTGGATACATCTGAAGCTGGACCGAAACCCAGATTTCACCGCTTCTTACAGATCCCT
 900
 V E Y I L K L D R N P O E T A S S Q I A
 TTCGGCTGGCGAGCTCAACCCATCAAGCAGCAGGGCGAAAGCGGTGCTTACCCGCTCTC

Fig 5A

901 ----- 900

Г Г Р А А Н Р М К О О Г О С Г А Ф Т Т Л

SEQ ID NO: 7
(Cont)

GAAGTTGCTCCATACtTGCTCTCCCCgGA/GAACTTGGAtGATCTGATCGCACTCGAAGTTC

[illegible]

SEQ ID No: 8
(cont)

E V A P Y L L S P E N L D D L I A P D V

TAA

1021 --- 1023

Fig 5B

SEQ ID NO: 9

ORF2 amino acid sequence

GTGGCCGAACAAGTTAAATTGAGCGTGGAGTTGATAGCGTGCAGTTCTTTTACTCCACCC

1 -----+-----+-----+-----+-----+-----+-----+ 60

SEQ ID NO: 10 M A E Q V K L S V E L I A C S S F T P

GCTGATGTTGAGTGGTCAACTGATGTTGAGGGCGCGTAGCACTCGTCGAGTTTGCGGGT

61 -----+-----+-----+-----+-----+-----+-----+ 120

A D V E W S T D V E G A E A L V E F A G

CGTGCCTGCTACGAACTTTTGATAAGCCGAACCTCGAACTGCTTCCAATGCTGCGTAT

121 -----+-----+-----+-----+-----+-----+-----+ 180

R A C Y E T F D K P N P R T A S N A A Y

CTGCGCCACATCATGGAAGTGGGGCACACTGCTTTGCTTGAGCATGCCAATGCCACGATG

181 -----+-----+-----+-----+-----+-----+-----+ 240

L R H I M E V G H T A L L E H A N A T M

TATATCCGAGGCATTTCTCGGTCCGCGACCCATGAATTGGTCCGACACCGCCATTTTCC

241 -----+-----+-----+-----+-----+-----+-----+ 300

Y I R G I S R S A T H E L V R H R H F S

TTCTCTCAACTGTCTCAGCGTTTCGTGCACAGCGGAGAATCGGAAGTAGTGGTGCCCACT

301 -----+-----+-----+-----+-----+-----+-----+ 360

F S Q L S Q R F V H S G E S E V V V F T

CTCATCGATGAAGATCCGCAGTTGCGTGAACCTTTTCATGCACGCCATGGATGAGTCTCGG

361 -----+-----+-----+-----+-----+-----+-----+ 420

L I D E D P Q L R E L F M H A M D E S R

TTGCGCTTTCATGAGCTGCTTAATGCGCTGGAAGAAAACTTGGCGATGAACCGAATGCA

421 -----+-----+-----+-----+-----+-----+-----+ 480

F A F N E L L N A L E E K L G D E P N A

CTTTTAAGGAAAAAGCAGGCTCGTCAAGCAGCTCGCGCTGTGCTGCCCAACGCTACAGAG

481 -----+-----+-----+-----+-----+-----+-----+ 540

L L R K K Q A R Q A A R A V L P N A T E

TCCAGAATCGTGGTGTCTGGAACTTCCGCACCTGGAGGCATTTTCATTGGCATGCGAGCC

541 -----+-----+-----+-----+-----+-----+-----+ 600

S R I V V S G N F R T W R H F I G M R A

AGTGAACATGCAGACGTCGAAATCCGCGAAGTAGCGGTAGGATGTTTAAGAAAGCTGCAG

601 -----+-----+-----+-----+-----+-----+-----+ 660

S E H A D V E I R E V A V G C L R K L Q

GTAGCAGCGCCAACTGTTTTCGGTGATTTTGAGATTGAACTTTGGCAGACGGATCGCAA

661 -----+-----+-----+-----+-----+-----+-----+ 720

V A A P T V F G D F E I E T L A D G S Q

ATGGCAACAAGCCCGTATGTCATGGACTTTTAA

721 -----+-----+-----+-----+-----+-----+ 753

M A T S P Y V M D F

Fig 6

Full length amino acid sequence of LysA (pRS6)

Seq ID No 11

ATGGCTACAGTTGAAAATTTCAATGAACITCCCGCACACGTATGGCCACGCAATGCCCGTG
1 -----+-----+-----+-----+-----+-----+-----+ 60

Seq ID No. 12

M A T V E N F N E L P A H V W P R : A V
CGCCAAGAAGACGGCGTTGTCACCGTCGCTGGTGTGCCTCTGCCTGACCTCGCTGAAGAA
61 -----+-----+-----+-----+-----+-----+-----+ 120
R Q E D G V V T V A G V P L P D L A E E
TACGGAACCCCACTGTTCCGTAGTCGACGAGGACGATTTCCGTTCCCGCTGTCGCGACATG
121 -----+-----+-----+-----+-----+-----+-----+ 180
Y G T P L F V V D E D D F R S R C R D M
GCTACCGCATTCCGGTGGACCAGGCAATGTGCACTACGCATCTAAAGCGTTCCTGACCAAG
181 -----+-----+-----+-----+-----+-----+-----+ 240
A T A F G G P G N V H Y A S K A F L T K
ACCATTGCACGTTGGGTTGATGAAGAGGGGCTGGCACTGGACATTGCATCCATCAACGAA
241 -----+-----+-----+-----+-----+-----+-----+ 300
T I A R W V D E E G L A L D I A S I N E
CTGGGCATTGCCCTGGCCGCTGGTTTCCCCGCCAGCCGTATCACCGCGCACGGCAACAAC
301 -----+-----+-----+-----+-----+-----+-----+ 360
L G I A L A A G F P A S R I T A H G N N
AAAGGCGTAGAGTTCCTGCGCGCGTTGGTTCAAAACGGTGTGGGACACGTGGTGGCTGGAC
361 -----+-----+-----+-----+-----+-----+-----+ 420
K G V E F L R A L V Q N G V G H V V L D
TCCGCACAGGAAGTAGAAGTGTGGATTACGTTGCCGCTGGTGAAGGCAAGATTCAAGGAC
421 -----+-----+-----+-----+-----+-----+-----+ 480
S A Q E L E L L D Y V A A G E G K : Q D
GTGTTGATCCGCGTAAAGCCAGGCATCGAAGCACACACCCACGAGTTCATCGCCACTAGC
481 -----+-----+-----+-----+-----+-----+-----+ 540
V L I R V K P G I E A H T H E F I A T S
CACGAAGACCAGAAGTTCGGATTCTCCCTGGCATCCGGTTCGGCATTGGAAGCAGCAAAA
541 -----+-----+-----+-----+-----+-----+-----+ 600
H E D Q K F G F S L A S G S A F E A A K
GCCGCCAACAACGCAGAAAACCTGAACCTGGTTGGCCTGCACTGCCACGTTGGTTCCCGAG
601 -----+-----+-----+-----+-----+-----+-----+ 660
A A N N A E N L N L V G L H C H V G S Q

Fig 7A

Lys A (pRS6)

Seq ID No 11 (cont)

Seq ID No 12

```

661. GTGTTTCGACGCCGAAGGCTTCAAGCTGGCAGCAGAACGCGTGTGGGCCTGTAATCACAG
-----+-----+-----+-----+-----+-----+-----+-----+-----+ 720
      V I D A E G F K L / A E P V L G L Y S Q
      ATCCACAGCGAACTGGGCGTTGCCCTTCTCTGAACCTGGATCTCGGTGGCGGATACGGCATT
721 -----+-----+-----+-----+-----+-----+-----+-----+ 780
      I H S E L G V A L P E L D L G G G Y G L
      GCCTATACCGCAGCTGAAGAACCACTCAACGTCGCAGAAGTTGCCTCCGACCTGCTCACC
781 -----+-----+-----+-----+-----+-----+-----+-----+ 840
      A Y T A A E E F L N V A E V A S D L L T
      GCAGTCGGAAAAATGGCAGCGGAACCTAGGCATCGACGCACCAACCGTGCTTGTGAGCCC
841 -----+-----+-----+-----+-----+-----+-----+-----+ 900
      A V G K M A A E L G I D A P T V L V E P
      GGCCGCGCTATCGCAGGCCCTCCACCGTGACCATCTACGAAGTCGGCACCACCAAAGAC
901 -----+-----+-----+-----+-----+-----+-----+-----+ 960
      G R A I A G P S T V T I Y E V G T T K D
      GTCCACGTAGACGACGACAAAACCCGCGTTACATCGCCGTGGACGGAGGCATGTCCGAC
961 -----+-----+-----+-----+-----+-----+-----+-----+ 1020
      V H V D D D K T R R Y I A V D G G M S D
      AACATCCGCCCAGCACTCTACGGCTCCGAATACGACGCCCGCGTAGTATCCCGCTTCGCC
1021 -----+-----+-----+-----+-----+-----+-----+-----+ 1080
      N I R P A L Y G S E Y D A R V V S R F A
      GAAGGAGACCCAGTAAGCACCCGCATCGTGGGCTCCCACTGCGAATCCGGCGATATCCTG
1081 -----+-----+-----+-----+-----+-----+-----+-----+ 1140
      E G D P V S T R I V G S H C E S G D I L
      ATCAACGATGAAATCTACCCATCTGACATCACCAGCGGCGACTTCCTTGCACTCGCAGCC
1141 -----+-----+-----+-----+-----+-----+-----+-----+ 1200
      I N D E I Y P S D I T S G D F L A L A A
      ACCGGCGCATACTGCTACGCCATGAGCTCCCGCTACAACGCCTTCACACGGCCCGCCGTC
1201 -----+-----+-----+-----+-----+-----+-----+-----+ 1260
      T G A Y C Y A M S S R Y N A F T R P A V
      GTGTCCGTCCGCGCTGGCAGCTCCCGCCTCATGCTGCGCCGCGAAACGCTCGACGACATC
1261 -----+-----+-----+-----+-----+-----+-----+-----+ 1320
      V S V R A G S S R L M L R R E T L D D I
  
```

Fig 7B

Lys A (pRS6)

(cont)

Seq ID 11 1321 CTCTCACTAGAGGCATAA 1338

Seq ID NO 12 L S L E A *

Fig 7C

Truncated ORF2
amino acid sequence

Seq ID No: 13 GTGGCCGAACAAGTTAAATTGAGCGTGGAGTTGATAGCGTGCAGTTCTTTTACTCCACCC
1 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 60

Seq ID No: 14 M A E Q V K L S V E L I A C S S E T E P
GCTGATGTTGAGTGGTCAACTGATGTTGAGGGCGCGGAAGCACTCGTCCGAGTTTGCGGGT
61 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 120
A D V E W S T D V E G A E A L V E F A G
CGTGCCCTGCTACGAAACTTTTGATAAGCCGAACCCTCGAACTGCTTCCAATGCTGCGTAT
121 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 180
R A C Y E T F D K P N P R T A S N A A Y
CTGCGCCACATCATGGAAGTGGGGCACACTGCTTTGCTTGAGCATGCCAATGCCACGATG
181 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 240
L R H I M E V G H T A L L E H A N A T M
TATATCCGAGGCATTTCTCGGTCCGCGACCCATGAATTGGTCCGACACCGCCATTTTTC
241 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 300
Y I R G I S R S A T H E L V R H R H F S
TTCTCTCAACTGTCTCAGCGTTTCGTGCACAGCGGAGAATCGGAAGTAGTGGTCCCCACT
301 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 360
F S Q L S Q R F V H S G E S E V V V P T
CTCAT ...
361 -----
L (1)

Fig 8

Sequence encoded in the HpaI-PvuII fragment containing the P1

SEQ ID NO:15

AACCGGTGTGGAGCCGACCATTCGCGAGGCTGCACTGCAACGAGGTCGTAGTTTTGGTACATGGCTTCTG
GCCAGTTCATGGATTGGCTGCCGAAGAAGCTATAGGCATCGCCACCAGGGCCACCGGAGTTACCGAAGAT
GGTGCCCGTGCTTTTCGCCTTGGGCAGGGACCTTGACAAAGCCCACGCTGATATCGCCAAGTGAGGGATCAG
AATAGTGCATGGGCACGTCGATGCTGCCACATTGAGCGGAGGCAATATCTACCTGAGGTGGGCATTCTTCC
CAGCGGATGTTTTCTTGCGCTGCTGCAGTGGGCATTGATACCAAAAAGGGGCTAAGCGCAGTCGAGGCGG
CAAGAACTGCTACTACCTTTTTTATTGTCGAACGGGGCATTACGGCTCCAAGGACGTTTGTCTTCTGGGTCA
GTTACCCCAAAAAGCATATACAGAGACCAATGATTTTTTATTAAAAAGGCAGGGATTGTTATAAGTATGG
GTCGTATTCTGTGCGACGGGTGTACCTCGGCTAGAATTTCTCCCATGACACCAG

Figure 9

ATCC 13032			50
N13			
ATCC 21529			
Consensus	KALVVQKYGG SSLESAERIR HVAERIVATK KAGNDVWVVC SAKGOTTDEL		
	51		100
ATCC 13032			
N13			
ATCC 21529			
Consensus	LELAHAVNPV PPAREMOMLL TAGERISNAL VAMAIESLGA EAQSFSGQA		
	101		150
ATCC 13032			
N13			
ATCC 21529			
Consensus	GVLTERHGN ARIVDVTPGR VREALDEGKI CIVAGFQGVN KETRDVTTLG		
	151		200
ATCC 13032			
N13			
ATCC 21529			
Consensus	RGGSDTTAVA LAAALNADVC EIYSOVDGVY TADPRIVPNA QZLEKUSFEE		
	201		250
ATCC 13032			
N13			
ATCC 21529			
Consensus	MLELAAVGSK ILVLRVVEYA RAFNVPLRVR SSYSNDPCTL IAGSMEDIPV		
	251		300
ATCC 13032			
N13			
ATCC 21529			
Consensus	EEAVLTGVAT DKSEAKVTVL GISDKPGEAA KVFALADAE INIDMVLQNV		
	301		350
ATCC 13032		S	G
N13		A	D
ATCC 21529		A	G
Consensus	SSVEDGTTDI TPTCPRADGR RAKELKKLQ VEGNWTNVLY DZQVGEVSLV		
	351		400
ATCC 13032			
N13			
ATCC 21529			
Consensus	GAGMKSHPGV TAEFMEALRD VNVNIELIST SEIRISVLIR EDDLDAARA		
	401	421	
ATCC 13032			
N13			
ATCC 21529			
Consensus	LHEQFQLGGE DEAVVYACTG R		

Fig 10

Fig 11a

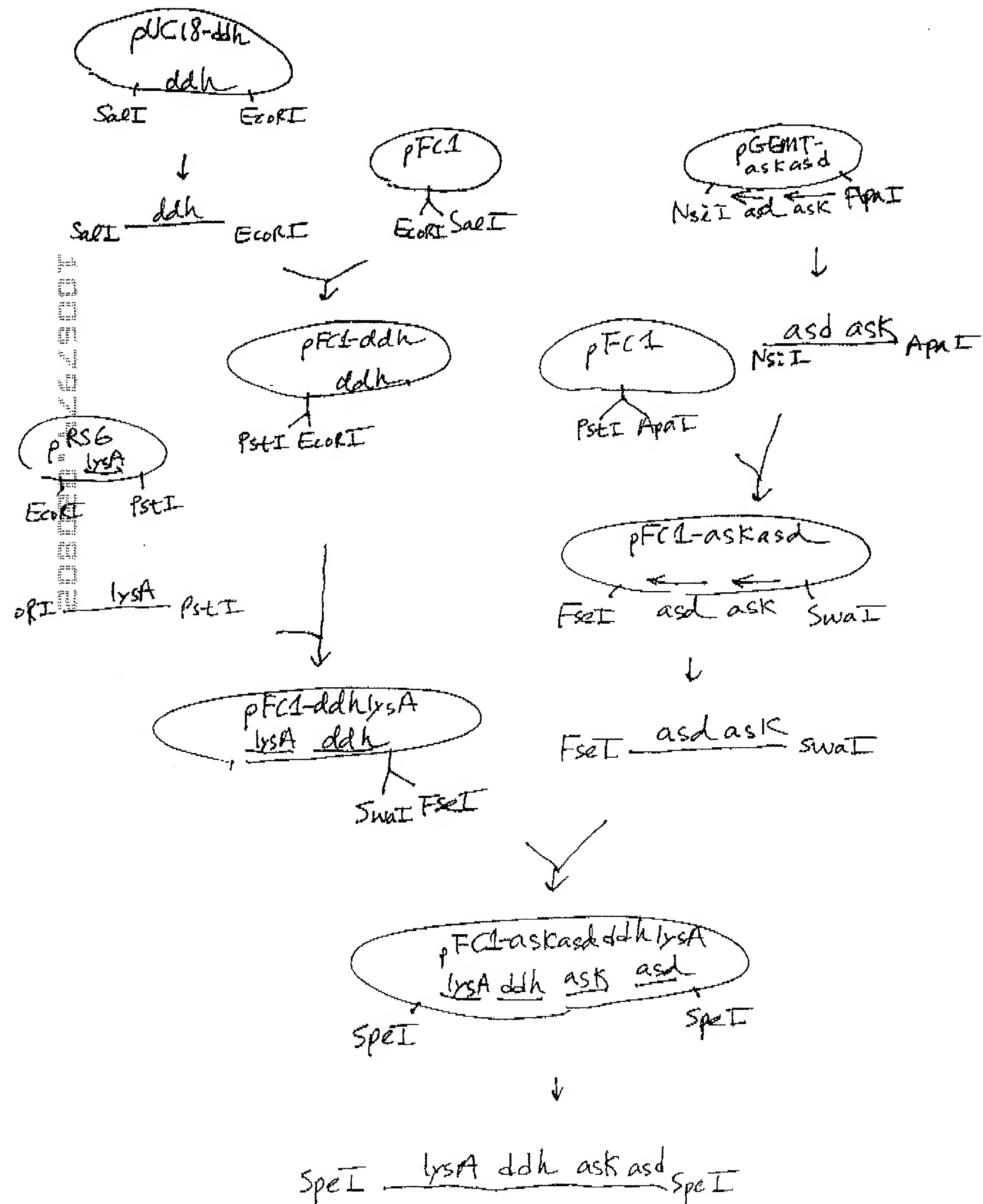
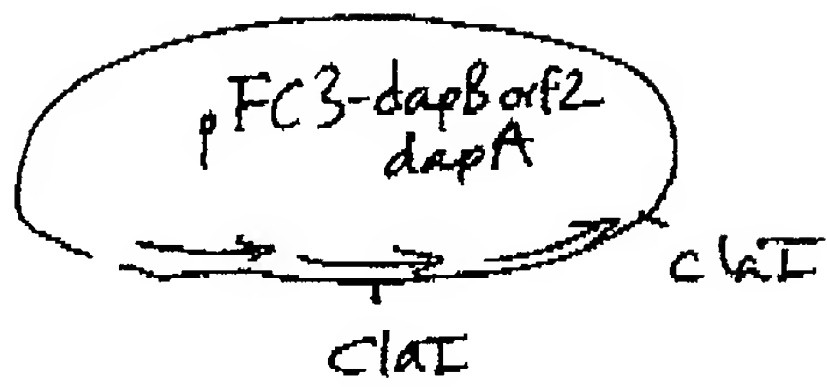
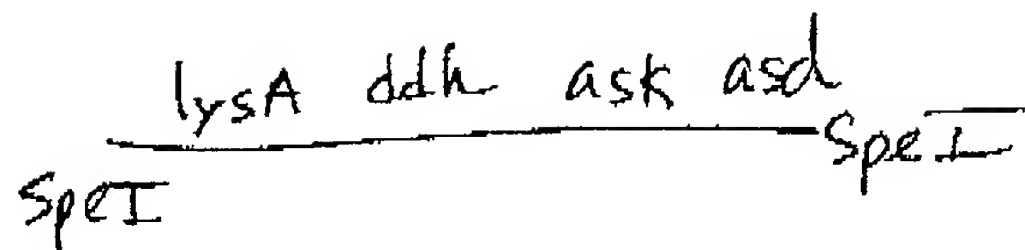
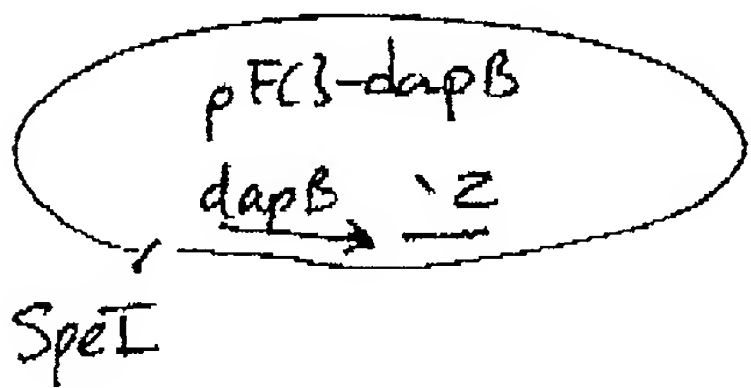


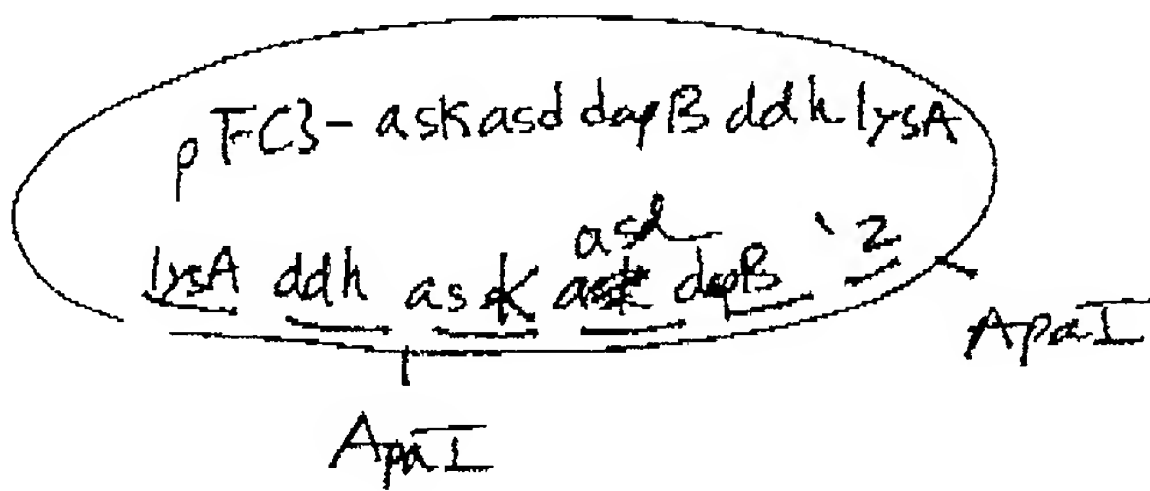
Fig 11 b



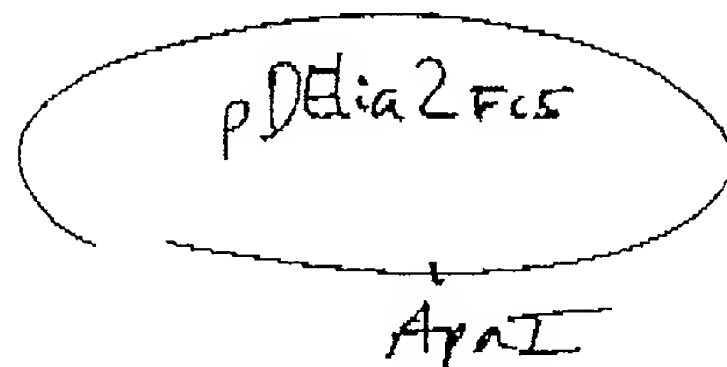
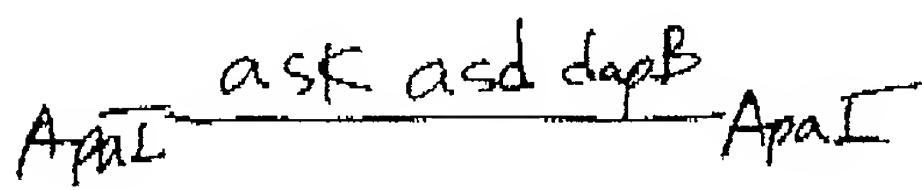
↓



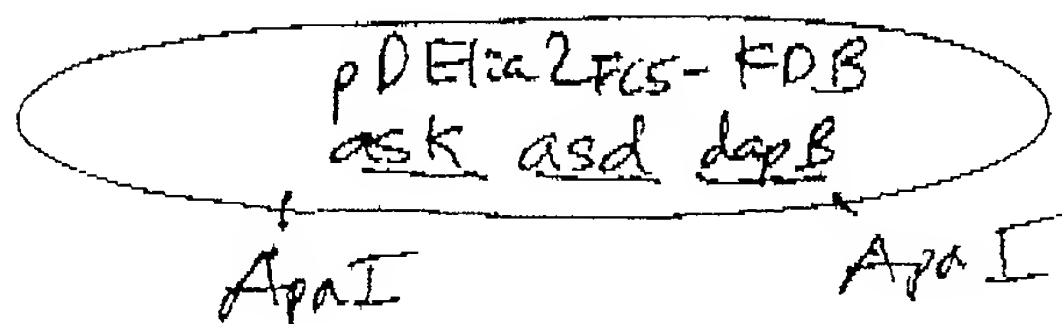
↘



↓



↘





NotI $\xrightarrow{\text{ask asd}}$ ApaI

↓ ClaI digestion; ligation

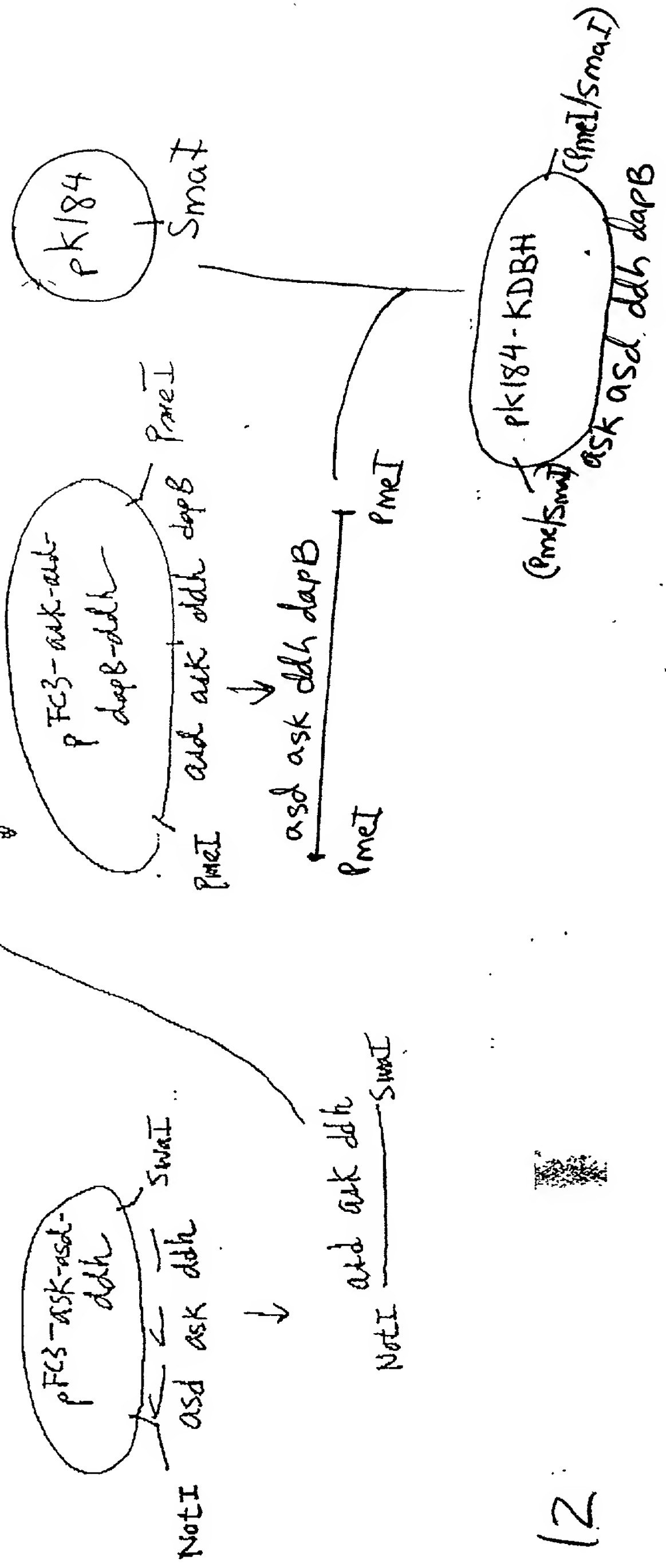
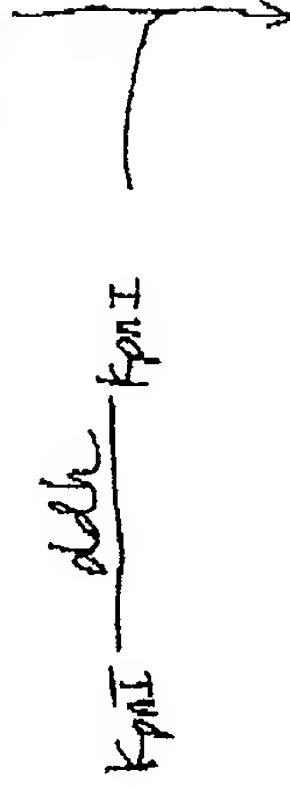
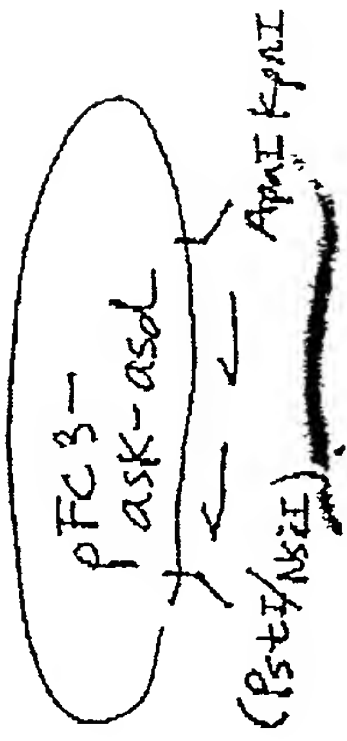


Fig 12

pDELia2_{FCS} - ask asd dapB orf2 (pDELia2_{FCS} - KDBZ)

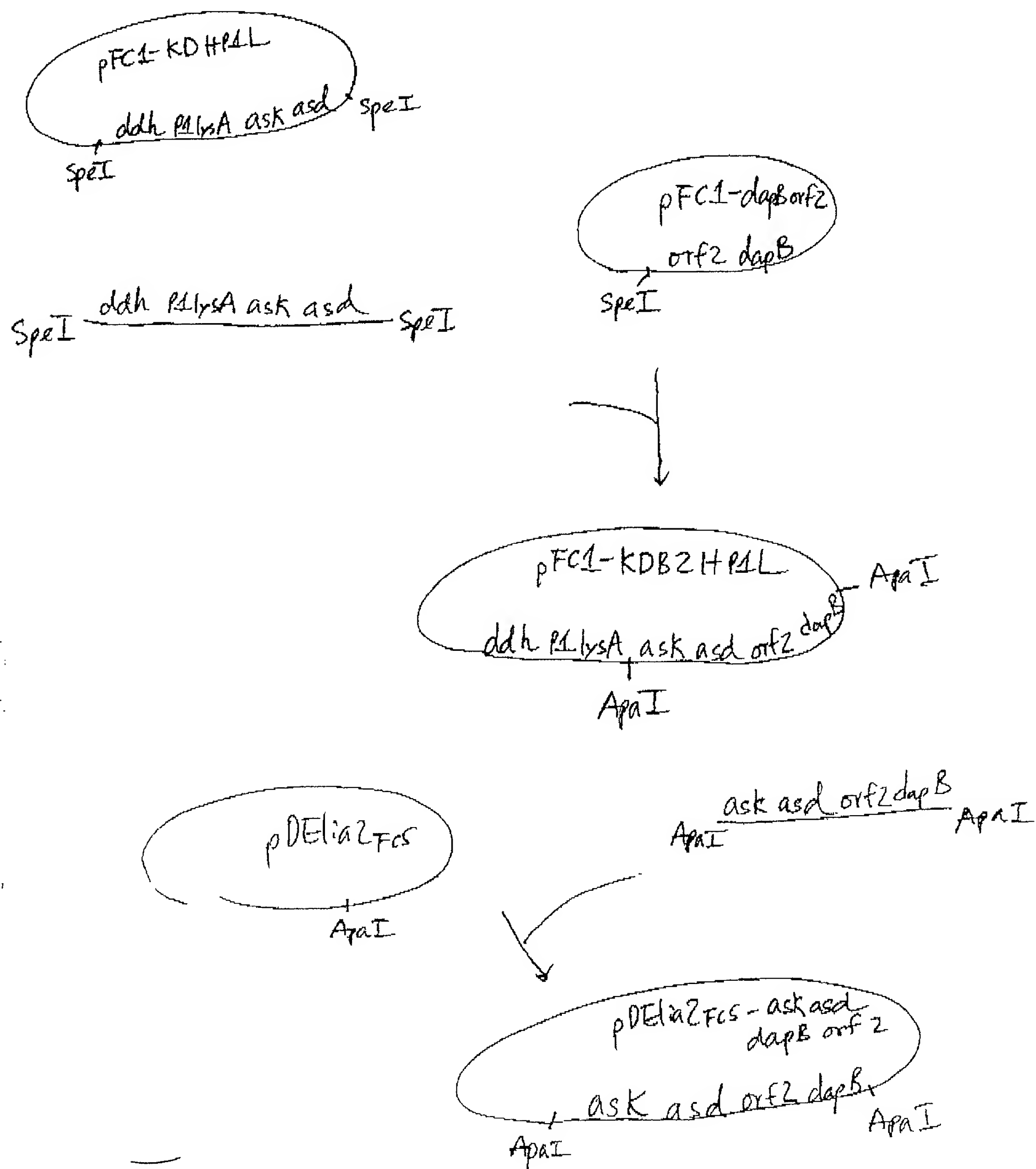


Fig 13

pDE1a 2 FCS - ask asd dapB orf2 ddh pLysA

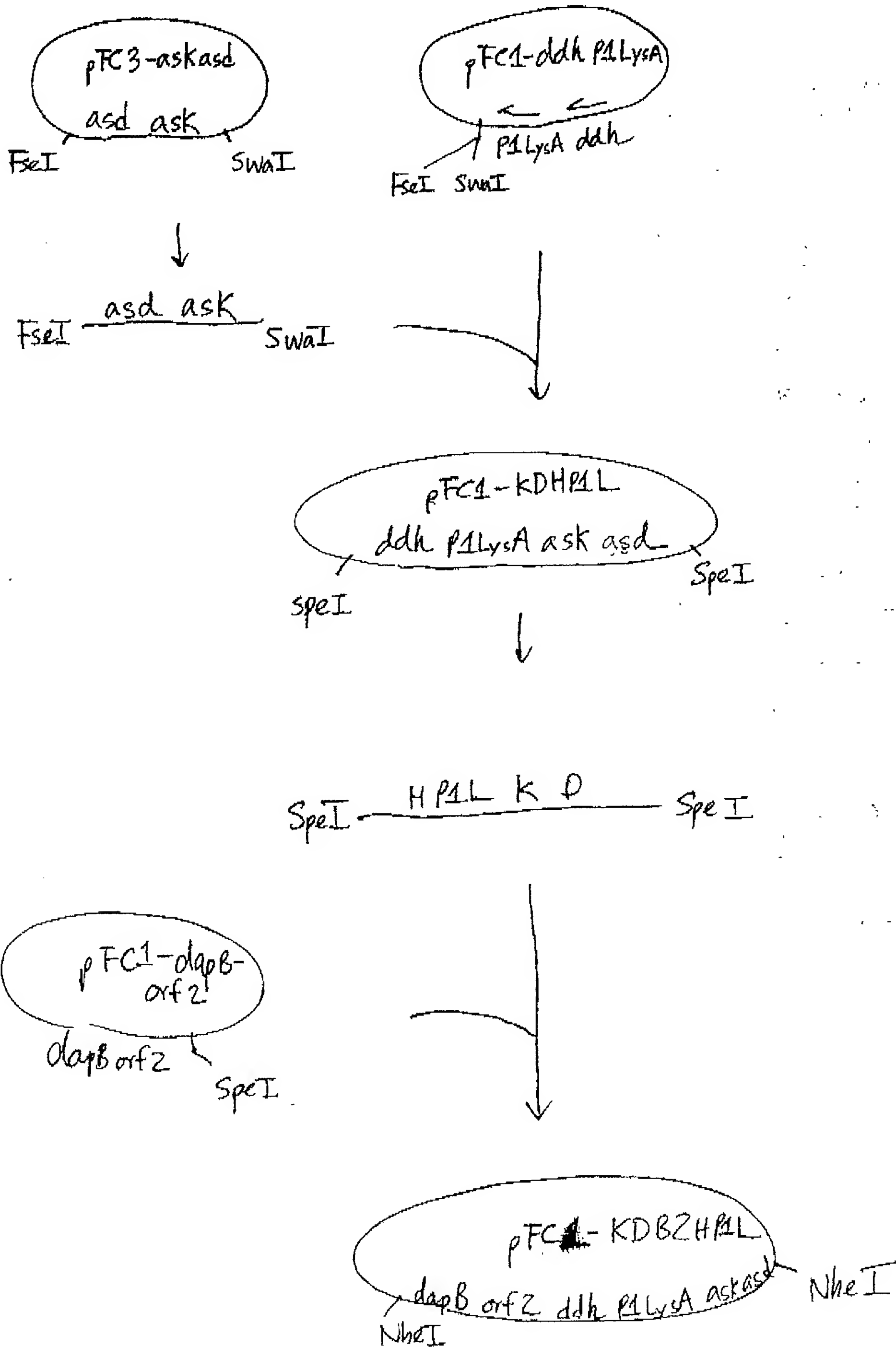


Fig. 24A

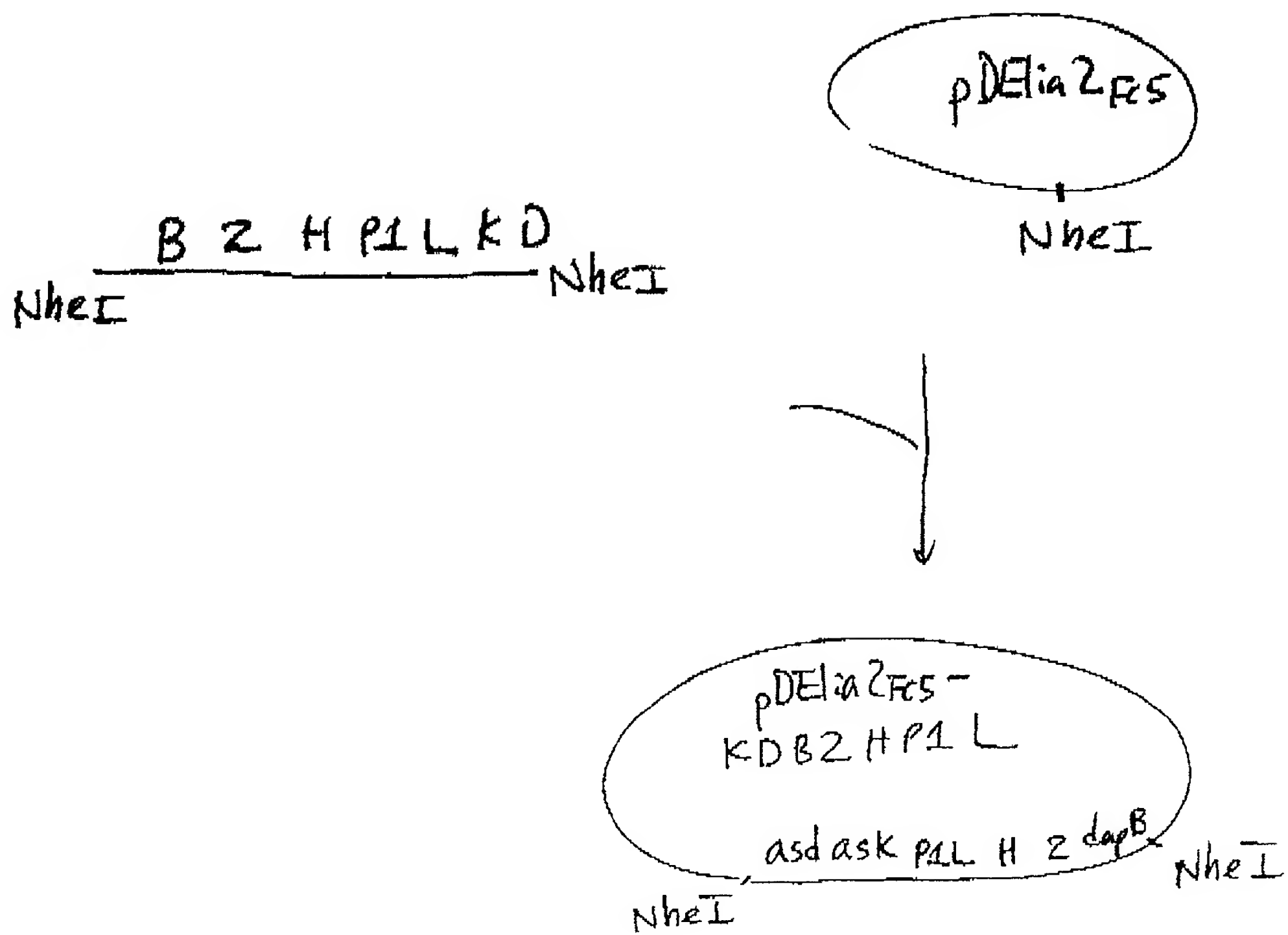


Fig. 14B